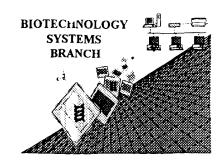
# RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/918,193
Source:	0196
Date Processed by STIC:	11/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

	CU ((A)) 102
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: (4/978, 193
ATTN: NEW RULES CASE	S: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOF
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in Patentln version 2.0 has caused fire <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
8Skipped Sequences (NEW'RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11 Use of <220>	Sequence(s) /57 missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

#### OIPE

RAW SEQUENCE LISTING DATE: 11/01/2001 PATENT APPLICATION: US/09/978,193 TIME: 10:47:23

Input Set : A:\Sequence\_Listing\_For\_P2630P1C6.wpd

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          Baker Kevin P.
  4
          Botstein, David
  5
          Desnoyers, Luc
  6
          Eaton, Dan
  7
          Ferrara, Napoleon
  8
          Filvaroff, Ellen
  9
          Fong, Sherman
 10
          Gao, Wei-Qiang
 11
          Gerber, Hanspeter
 12
          Gerritsen, Mary E.
 13
          Goddard, Audrey
 14
          Godowski, Paul J.
 15
          Grimaldi, J. Christopher
 16
          Gurney, Austin L.
 17
          Hillan, Kenneth J
 18
          Kljavin, Ivar J.
 19
          Kuo, Sophia S.
 20
          Napier, Mary A.
 21
          Pan, James;
 22
          Paoni, Nicholas F.
 23
          Roy, Margaret Ann
 24
           Shelton, David L.
 25
 26
           Stewart, Timothy A.
 27
          Tumas, Daniel
          Williams, P. Mickey
 28
          Wood, William I.
 29
 31 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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  34 <130> FILE REFERENCE: P2630P1C6
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PATENT APPLICATION: US/09/978,193

DATE: 11/01/2001 TIME: 10:47:23

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PATENT APPLICATION: US/09/978,193

DATE: 11/01/2001 TIME: 10:47:23

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PATENT APPLICATION: US/09/978,193

DATE: 11/01/2001 TIME: 10:47:23

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PATENT APPLICATION: US/09/978,193

DATE: 11/01/2001 TIME: 10:47:23

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### VERIFICATION SUMMARY

PATENT APPLICATION: US/09/978,193

DATE: 11/01/2001 TIME: 10:47:24

Input Set : A:\Sequence\_Listing\_For\_P2630P1C6.wpd

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L:36 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:244 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:370 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:445 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
\rm L\!:\!992\ M\!:\!341\ W\!: (46) "n" or "Xaa" used, for SEQ ID#:8
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L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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#### VERIFICATION SUMMARY

PATENT APPLICATION: US/09/978,193

DATE: 11/01/2001 TIME: 10:47:24

Input Set : A:\Sequence\_Listing\_For\_P2630P1C6.wpd

Output Set: N:\CRF3\11012001\1978193.raw

 $L:6387\ M:220\ C:\ Keyword\ misspelled\ or\ invalid\ format,\ <213>\ ORGANISM\ for\ SEQ\ ID#:157$  $L:6389\ M:258\ W:$  Mandatory Feature missing, <220> FEATURE: L:6389 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:7713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191

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 $L:10657 \ M:341 \ W: (46) \ "n" \ or "Xaa" \ used, for SEQ ID#:265$